

Db	1	MAFN	DL	LK	QV	GG	VR	GR	FQ	L	I	Q	V	T	M	V	A	P	L	L	M	A	S	H	N	T	L	Q	N	F	T	A	A	I	P	H	H	C	R	P	P	A	N	A	N	L	S	K	D	60												
Qy	61	GG	LE	VW	L	P	R	D	R	Q	Q	P	E	S	C	L	R	F	T	S	P	Q	W	G	L	P	F	L	N	G	T	E	A	N	G	T	G	A	T	E	P	C	T	D	G	W	I	Y	D	N	S	T	F	P	S	T	I	120				
Db	61	GG	LE	AW	L	P	L	D	K	Q	Q	P	E	S	C	L	R	F	T	S	P	Q	W	G	P	P	F	Y	N	G	T	E	A	N	G	T	R	V	T	E	P	C	I	D	G	W	Y	D	N	S	T	F	P	S	T	I	120					
Qy	121	V	T	E	W	D	L	V	C	S	H	R	A	L	R	Q	L	A	Q	S	L	Y	M	V	G	V	L	L	G	A	M	V	F	G	Y	L	A	D	R	L	G	R	R	K	V	L	I	N	Y	L	Q	T	A	V	S	G	T	C	A	A	180	
Db	121	V	T	E	W	N	L	V	C	S	H	R	A	F	R	Q	L	A	Q	S	L	Y	M	V	G	V	L	L	G	A	M	V	F	G	Y	L	A	D	R	L	G	R	R	K	V	L	I	N	Y	L	Q	T	A	V	S	G	T	C	A	A	180	
Qy	181	F	A	P	N	F	P	I	Y	C	A	F	R	L	L	S	G	M	A	L	A	G	I	S	L	N	C	M	T	L	N	V	E	W	M	P	I	H	T	R	A	C	V	G	T	L	I	G	Y	V	Y	S	L	G	Q	F	L	L	A	G	V	240
Db	181	Y	A	P	N	Y	T	V	Y	C	V	F	R	L	L	S	G	M	S	L	A	S	I	A	I	N	C	M	T	L	N	V	E	W	M	P	I	H	T	R	A	Y	V	G	T	L	I	G	Y	V	Y	S	L	G	Q	F	L	L	A	G	I	240
Qy	241	A	Y	A	V	P	H	R	H	L	Q	L	L	V	S	A	P	F	F	A	F	F	I	Y	S	W	F	F	I	E	S	A	R	W	H	S	S	S	G	R	L	D	L	T	L	R	A	L	Q	R	V	A	R	I	N	G	K	R	E	E	300	
Db	241	A	Y	A	V	P	H	R	H	L	Q	L	V	S	V	P	F	F	I	A	F	I	Y	S	W	F	F	I	E	S	A	R	W	Y	S	S	S	G	R	L	D	L	T	L	R	A	L	Q	R	V	A	R	I	N	G	K	Q	E	E	300		
Qy	301	G	A	K	L	S	M	E	V	L	R	A	S	L	Q	K	E	L	T	M	G	K	G	Q	A	S	A	M	E	L	L	R	C	P	T	L	R	H	L	F	L	C	L	S	M	L	W	F	A	T	S	F	A	Y	Y	G	L	V	M	D	L	360
Db	301	G	A	K	L	S	I	E	V	L	R	T	S	L	Q	K	E	L	T	S	K	G	Q	A	S	A	M	E	L	L	R	C	P	T	L	R	H	L	F	L	C	L	S	M	L	W	F	A	T	S	F	A	Y	Y	G	L	V	M	D	L	360	
Qy	361	Q	G	F	G	V	S	I	Y	L	I	Q	V	I	F	G	A	V	D	L	P	A	K	L	V	G	F	L	V	I	N	S	L	G	R	R	P	A	Q	M	A	L	L	L	A	G	I	C	I	L	L	N	G	V	I	P	Q	D	Q	S	420	
Db	361	Q	G	F	G	V	S	M	Y	L	I	Q	V	I	F	G	A	V	D	L	P	A	K	F	V	C	F	L	V	I	N	S	M	G	R	R																										

Sequence Comparison A

RESULT 6

O35956

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ID   O35956      PRELIMINARY;      PRT;    551 AA.
AC   O35956;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Renal organic anion transport protein 1.
GN   SLC22A6 OR ROAT1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC   TISSUE=KIDNEY;
RX   MEDLINE=98043701; PubMed=9374486;
RA   Sweet D.H., Wolff N.A., Pritchard J.B.;
RT   "Expression cloning and characterization of ROAT1. The basolateral
RT   organic anion transporter in rat kidney.";
RL   J. Biol. Chem. 272:30088-30095(1997).
RN   [2]
RP   SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=KIDNEY;
RX   MEDLINE=97373539; PubMed=9228014;
RA   Sekine T., Watanabe N., Hosoyamada M., Kanai Y., Endou H.;
RT   "Expression cloning and characterization of a novel multispecific
RT   organic anion transporter.";
RL   J. Biol. Chem. 272:18526-18529(1997).
CC   -!- FUNCTION: MEDIATES THE NA(+)-INDEPENDENT TRANSPORT OF ORGANIC
CC   ANIONS SUCH AS CYCLIC NUCLEOTIDES, PROSTAGLANDIN E2 AND URIC ACID.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. BASOLATERAL
CC   MEMBRANE (POTENTIAL).
CC   -!- TISSUE SPECIFICITY: STRONG EXPRESSION IN KIDNEY. VERY WEAK
CC   EXPRESSION IN BRAIN. NOT DETECTED IN HEART, LUNG, LIVER, SPLEEN
CC   SKELETAL MUSCLE, SMALL INTESTINE, LARGE INTESTINE, EYE OR TESTIS.
CC   EXPRESSED IN THE PROXIMAL TUBULE IN THE KIDNEY.
CC   -!- PTM: GLYCOSYLATED (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE SLC22 FAMILY OF TRANSPORTERS.
DR   EMBL; AF008221; AAC18772.1; -.
DR   EMBL; AB004559; BAA22086.1; -.
DR   InterPro; IPR007114; MFS.
DR   InterPro; IPR004749; Orgcat_transp.
DR   InterPro; IPR005828; Sub_transporter.
DR   Pfam; PF00083; sugar_tr; 1.
DR   TIGRFAMs; TIGR00898; 2A0119; 1.
DR   PROSITE; PS50850; MFS; 1.
KW   Transmembrane; Transport; Glycoprotein; Ion transport.
FT   TRANSMEM      136      156      POTENTIAL.
FT   TRANSMEM      196      216      POTENTIAL.
FT   TRANSMEM      249      269      POTENTIAL.
FT   TRANSMEM      338      358      POTENTIAL.
FT   TRANSMEM      396      416      POTENTIAL.
FT   TRANSMEM      485      505      POTENTIAL.
FT   CARBOHYD       39       39      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD       56       56      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD       92       92      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      113      113      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      184      184      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE      551 AA;  60766 MW;  8BA47BE628324BF2 CRC64;
  
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Query Match 89.5%; Score 2549.5; DB 11; Length 551;
 Best Local Similarity 87.8%; Pred. No. 1.5e-203;
 Matches 484; Conservative 35; Mismatches 31; Indels 1; Gaps 1;

QY 1 MAFNDLLQQVGGVGRFQQIQVTLVVLP LLLMASHNTLQNF TAAIPTHHCRPPADANLSKN 60
 |||||:|||||: |||:| |||||:|||||: |||||:|||||: